AL:EAG/MSM
F. # 2014R01047

UNITED STATES DISTRICT COURT
EASTERN DISTRICT OF NEW YORK

– –X

UNITED STATES OF AMERICA

- against - Docket No. 14–CR-414 (BMC)

RASHAWN JERMAINE SMALLS,

Defendant.

– –X

AFFIDAVIT OF CRAIG O'CONNOR

I, DR. CRAIG O'CONNOR, pursuant to 28 U.S.C. § 1746, declare as follows:

BACKGROUND

1. I am a Criminalist IV and Assistant Technical Leader for Nuclear DNA Operations in the Department of Forensic Biology at the New York City Office of Chief Medical Examiner ("OCME") and a Clinical Assistant Professor in the Department of Forensic Medicine at New York University Medical Center.

2. I have a Bachelor's of Science in physiology and neurobiology from the University of Connecticut. Prior to attending graduate school, I spent a year and a half as a research technician at the Yale University School of Medicine performing biochemical assays dealing with uterine and prostate cancer. In 2007, I received a Master's of Science and in 2008 a Ph.D both in genetics and genomics from the University of Connecticut. During graduate school, my research focused on forensic human identification. In 2008, I began working at the OCME.

3. As an OCME Criminalist, my main duties include the day-to-day examination of evidence from crimes such as homicides, assaults, sexual assaults, property crimes and cold cases, DNA analysis, writing reports and testifying in court.

Determining the Number of Contributors to a Sample

4. The OCME has developed guidelines, or protocols, that are used to estimate the number of contributors in a mixture and are included within a document entitled "Forensic Biology Protocols for Forensic STR Analysis" (the "Protocols"). The portion of the Protocols that are used to estimate the number of contributors in a mixture notes that its purpose "is to provide a framework which can be applied to the interpretation of STR results in casework. The guidelines are based on validation studies, literature references, some standard rules and experience. However, not every situation can be covered by a pre-set rule. Equipped with these guidelines, analysts should rely on professional judgment and expertise." Protocols at 404. (An excerpt of the Protocols that is used to determine the number of contributors in a mixture is attached as Exhibit A.)

5. The Protocols provide that "[a] minimum number of contributors to a mixed profile can be estimated using the locus or loci demonstrating the largest number of labeled peaks." Id. at 411. The Protocols further provide that a mixture should be characterized as a three-person mixture when "[f]ive alleles (repeating or non-repeating) are present at at least two loci" and caution that "[s]tutter and other explainable artifacts should be considered when counting the number of alleles at a locus." Id. at 412. By contrast, the Protocols provide that "samples that show seven or more labeled peaks (repeating or non-repeating) at two or more STR loci" are indicative of four-person mixtures and therefore not suitable for FST at this time. See id. at 407.

6. It is not possible to definitively determine the number of contributors to a mixture based solely on the number of alleles present because, in part, a mixture may contain alleles that do not belong to any contributor, but instead are "artifacts" resulting from, for example, stutter or drop-in.[1] A stutter is an artifact that results from the amplification process. To be conservative, and unlike other types of artifacts such as the "dye blob" and "pull up," a stutter that is not automatically removed by the GeneMapper stutter filter cannot be removed from a mixture because the analysts are unable to determine whether it is a true stutter or a peak from a very minor contributor to the mixture. Drop-in is often attributable to contamination of the sample or the testing equipment or from a very minor contributor's DNA that may have been on the item. An allele that is present in multiple runs (i.e., a repeating allele) is less likely to be the result of stutter or drop-in.

7. A research study was performed by the OCME "[t]o develop guidelines to estimate the number of contributors to two-, three-, and four-person mixtures containing either high template DNA (HT-DNA) or low template DNA (LT-DNA) amounts" (the "Perez Study"). J. Perez et al., "Estimating the number of contributors to two-, three-, and four-

[1] The GeneMapper program takes several steps to minimize these artifacts. First, an analytical threshold is applied to help separate "real" peaks from "noise" or "static." OCME uses a threshold setting of 75 RFUs and, as a result, GeneMapper will only label peaks that are 75 RFUs or more. Second, a ten percent general filter is applied. As a result of this filter, GeneMapper will not label peaks that are less than ten percent of the tallest peak at each locus. Third, a "stutter filter" specific to each locus is applied. As a result, with respect to each locus, GeneMapper will not label peaks in the "stutter position" for that locus if the peaks are less than a specified percentage of the highest peak at that locus. The locus-specific stutter filters were validated using samples with 500 picograms of DNA. The presence of stutter and other stochastic effects, however, increases as the amount of DNA in the sample decreases. Where, as here, the sample contains less than 500 picograms of DNA, there is an increased chance that the "stutter filters" will not remove all of the peaks attributable to stutter.

person mixtures containing DNA in high template and low template amounts," Croat. Med. J. (2011) at 314. (A copy of the Perez Study is attached as Exhibit B.)

8. The authors of the Perez Study commented that "[i]nterpretation guidelines from the Scientific Working Group on DNA Analysis Methods specify that the minimum number of contributors to a mixture can be determined based on the locus that exhibits the greatest number of peaks, with an allowance for tri-allelic loci and/or stutter. Following these allele-counting guidelines, a sample with 3 or more labeled alleles at 1 or more loci can be considered to contain a minimum of 2 contributors, a sample with 5 or more labeled alleles at 1 or more loci can be considered to contain a minimum of 3 contributors, and so on." Id. at 315. The authors of the Perez Study further noted that "[e]mpirical analysis of conceptual mixtures of individuals typed at 13 loci estimated that using the maximum number of alleles observed at any locus, 3.2%-3.4% of three-person mixtures would be categorized as mixtures of at least 2 people" citing an article entitled "Empirical analysis of the STR profiles resulting from conceptual mixtures" in the Journal of Forensic Science by David R. Paoleti, et al. ("Paoletti Study"). Id. (A copy of the Paoletti Study is attached as Exhibit C.) Because the Paoletti Study was conceptual in nature and did not examine any samples in a laboratory, the Paoletti Study did not account for the presence of stutter or drop in.

9. In contrast with the Paoletti study, in the Perez Study, 728 purposeful mixed samples in a laboratory of "varying template amounts, and numbers and ratios of contributors were examined." Id. at 319. Of the 728 mixed samples, 355 were samples with 100 picograms or more of DNA; the remaining 373 samples were for 100 picograms or less of DNA. Id. at 317. Of the 355 mixed samples (i.e., the high-template samples), 184 were from two persons, 121 were from three persons, and 50 were from four persons; the mixture ratios varied

as follows: 1:1 (n = 50), 2:1 (n = 34), 4:1 (n = 100), 1:1:1 (n = 18), 2:2:1 (n = 1), 3:1:1 (n = 20), 4:1:1 (n = 6), 5:1:1 (n = 63), 5:5:1 (n = 13), 1:1:1:1 (n = 23), 5:1:1:1 (n = 2), 4:1:1:1; (n = 1), 3:1:1:1 (n = 1), 2:1:1:1 (n = 1), 4:3:2:1 (n = 6), 3:2:1:1 (n = 5), 3:3:2:2 (n = 5), and 2:2:1:1 (n = 6). Id. at 317.

10. In the Perez Study, the authors concluded that "the results of [the Perez Study] suggest that samples with 49 or fewer alleles are best described as two[-]person mixtures, with 52 to 59 alleles as three-person mixtures, and with 65 or more alleles as four-person mixtures."[2] Id. at 318. However, in the Perez study itself, at least one three-person mixture contained a total of 66 alleles and one four-person mixture contained 57 alleles. Id. at 318, Table 1. The authors of the Perez study therefore concluded that the presence of 57 to 66 alleles "warranted additional scrutiny." Id. at 321. In any event, it is theoretically possible for a two-person mixture to contain up to 60 alleles and a three-person mixture to contain up to 90 alleles.[3]

11. The Perez Study also identified nine characteristics that distinguished three-person from two-person mixtures and eight characteristics that distinguished four-person from three-person mixtures, which characteristics were set forth in Table 2 of the Perez Study. Id. at 318. The results contained in Table 2 that are applicable to samples with 100 picograms or more of DNA (i.e., high-template DNA) are set forth below.

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[2] These numbers were developed based on the mean of the number of alleles present at all loci over all runs for the purposeful mixtures of two-, three- and four-persons plus or minus two standard deviations. See Perez Study at 318, Table 1.

[3] The OCME identifies the alleles present at 15 different loci.

Characteristics that Tend to Distinguish Three-person from Two-person Mixtures:	Characteristics that Tend to Distinguish Four-person from Three-person Mixtures:
• ≥2 loci with ≥5 repeating alleles	• ≥2 loci with ≥7 repeating alleles
• ≥2 different loci with ≥5 alleles in one replicate	• ≥3 loci with ≥6 repeating alleles
• ≥8 loci with ≥4 repeating alleles	• ≥6 loci with ≥5 repeating alleles
• 1 locus with ≥5 repeating alleles and ≥1 other loci with ≥5 different alleles	• ≥12 loci with ≥4 repeating alleles
• ≥1 locus with 7 different alleles	• ≥2 loci with ≥7 different alleles
• ≥2 loci with 6 different alleles	• ≥3 loci with ≥6 different alleles
• 1 locus with 6 different alleles and ≥3 loci with 5 different alleles (LT-DNA)	• ≥7 loci with ≥5 different alleles
• ≥4 loci with ≥5 different alleles	• ≥13 loci with ≥4 different alleles
• ≥8 loci with ≥4 different alleles[4]	• not applicable

12. I have reviewed a report dated January 9, 2014, setting forth the results obtained from PCR DNA testing on evidence contained in NYPD voucher number 4000177476. That voucher contained three swabs that were taken from a .25 caliber Raven Arms pistol, model MP-25, serial number 740272 (the "Raven Arms firearm"), including a swab from the "entire grip area" of the Raven Arms firearm. A copy of the January 9, 2014 report is attached as Exhibit D. I have also reviewed copies of the electropherograms for the "entire grip area" of the Raven Arms firearm, which are attached as Exhibits E, F and G. Exhibits E and F represent the electropherograms created from the first run; Exhibit G

[4] The authors of the Perez Study noted that "[o]ne two-person mixture with 100 picograms or less of DNA had 8 loci with 4 or 5 different alleles. The additional alleles could be attributed to stutter." Perez Study at 318.

represents the electropherograms created from the second run. Finally, I have reviewed a report titled "Forensic Statistical Comparison Report," which documents the statistical comparison using the Likelihood Ratio of the DNA data from the swab from the "entire grip area" of the Raven Arms firearm to the DNA profile from an individual named Rashawn Smalls. A copy of that report is attached as Exhibit H.

13. A review of the alleles identified at each locus shows that in the first run, there were five or more alleles at six loci (D8S1179, D21S11, D3S1358, D19S433 and vWA), and in the second run, there were five or more alleles at only three loci (D13S317, D19S433 and vWA). A review of those alleles shows that there were seven alleles (10, 11, 12, 13, 14, 14.2, 16.2) in only one locus (D19S433 in run two).

14. Two of the alleles in the first run, 16 at D8S1179 and 10 at D16S539, and one of the alleles in the second run, 13 at D5S818, may be the result of stutter. Stutter may occur where there is an allele with a relative florescence unit peak ("RFU peak") that is a small percentage of the RFU peak for an allele that is one greater or one lesser repeat unit than the other true allele. In the first run, at D8S1179, the RFU peak for the 16 allele (i.e., 189 in Run 1a and 162 in Run 1b) is in a stutter position and it is approximately 13% of the RFU peak for the 15 allele (i.e., 1442 in Run 1a and 1187 in Run 1b); as a result, the 16 may be the result of stutter rather than a true allele that contributed to the mixture.[5] See Exhibits E (Run 1a) and F (Run 1b). Also in the first run, at D16S539, the RFU peak for the 10 allele (i.e., 78) in a stutter position and it is approximately 15% of the RFU peak for the 11 allele (i.e., 508); as a result, the 10 may be the result of stutter rather than a true allele that

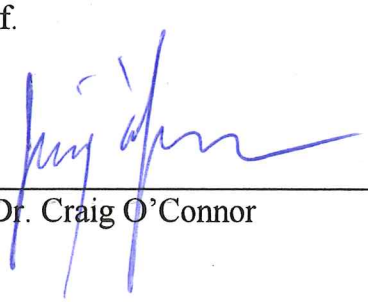
[5] Run 1 was run twice because in Run 1a (see Exhibit E) at FGA, an allele was identified that was "off ladder" or OL. In Run 1b (see Exhibit F), the "OL" allele did not appear again and therefore was not confirmed as a true allele.

contributed to the mixture. See Exhibit E (Run 1a). In the second run, at D5S818, the RFU peak for the 13 allele (i.e., 124) is in a stutter position and it is approximately 15% of the RFU peak for the 12 allele (i.e., 810); as a result, the 13 may be the result of stutter rather than a true allele that contributed to the mixture. See Exhibit G (Run 2).

15. In fact, six of the nine characteristics identified by the authors of the Perez Study as indicative of three-person samples were present in the mixture at issue, and only three of the eight characteristics identified by the authors of the Perez Study as indicative of four-person mixtures was present in the mixture at issue.

16. While 69 different alleles appeared over the two runs, the analyst used proper discretion in classifying this as an estimated three-person – rather than four-person – mixture. As an initial matter, if the three alleles noted in paragraph 14 were stutter rather than true alleles, there would only be 66 alleles that appeared over the two runs that were true contributors to the mixture. In reviewing the alleles detected in the entire profile – and not just at one locus – and considering stutter and other phenomenon, it is more cautious to classify this mixture as containing at least three contributors rather than at least four contributors.

17. I declare under penalty of perjury that the foregoing is true and correct to the best of my knowledge, information and belief.



Dr. Craig O'Connor

Dated: June 5, 2015
New York, New York